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A SIMPLE BATCH EPIDEMIC PROCESS

by

L. Billard¹, H. Lacayo² & N. A. Langberg

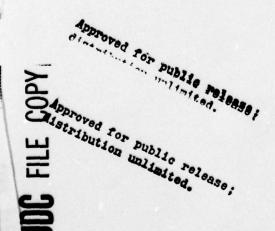
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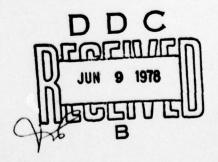
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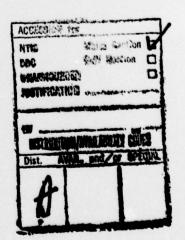
A Simple Batch Epidemic Process

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L. Billard, H. Lacayo & N. A. Langberg Florida State University

SUMMARY

A simplifying assumption for an epidemic process is that at most one person may become infected at any one time. However, it is quite conceivable that when an infected person makes simultaneous contact with two people, both could become infected. In this note we introduce the concept of a batch epidemic process in which infection can occur in batches of one or two. The distribution of the number of infectives present at any time is derived. The concept can be extended to include batches of any size.



1. INTRODUCTION

The simple epidemic model describes the process in which a population of fixed size N consists of susceptibles and infectives. A basic assumption is that at any particular instant in time at most one susceptible individual can become infected. However, it is quite conceivable that when an infected person makes simultaneous contact with two people both could become infected. More generally, susceptibles could become infectives in batches of any size. For simplicity, we shall consider here the case in which infection occurs in batches of one or two with probability α and $(1 - \alpha)$ respectively.

Let X(t) denote the number of infectives at time t. The infinitesimal transition rates for our model are given by

$$Pr\{X(t+h) = x + 1|X(t) = x\} = \alpha\mu_X h + o(h)$$

$$Pr\{X(t+h) = x + 2|X(t) = x\} = (1 - \alpha)\mu_X h + o(h)$$
and
$$Pr\{X(t+h) = x|X(t) = x\} = 1 - \mu_X h + o(h)$$
(1)

where μ_X , $x = 1, \ldots, N$, are arbitrary but distinct infection rates. In the classical simple epidemic model, $\alpha \equiv 1$ and $\mu_X \equiv \beta x (N - x)$ where β is the rate of infection. In this work we find expressions for the probability distribution of X(t) for the above simple batch epidemic process. Note that the underlying model, from (1), satisfies the Chapman-Kolmegorov equations

$$p_n^*(t) = -\mu_n p_n(t) + \alpha \mu_{n-1} p_{n-1}(t) + (1 - \alpha) \mu_{n-2} p_{n-2}(t), \qquad (2)$$

for $n = 1, \ldots, N$ with $\mu_n = 0$ for $n \ge N$ or n < 1 and where

$$p_n(t) = Pr(X(t) = n)$$

2. SOME PRELIMINARIES

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Recently, Billard Lacayo and Langberg (1979) found a compact derivation for the classical simple epidemic process by focusing on the interinfection time between successive occurrences of infectives. The probability distribution for the number of infectives present at any time t was expressed in terms of a linear combination of exponential terms with parameters (μ_{χ} t) where μ_{χ} is defined as in Section 1. Since in the classical model infectives occur in batches of one only, the path followed by successively occuring values of χ is simply 1, 2, ..., N. However, when infectives can occur in batches of one or two, there are many possible paths that can be followed. Accordingly, we introduce some notation to describe the path possibilities.

Let μ_1, \ldots, μ_n be distinct positive real numbers. Define M(n, i, j) as the set of all subsets of $\{\mu_{i+1}, \ldots, \mu_{n-1}\}$ with j of them deleted but such that no two deleted elements have consecutive subscripts. Thus, for example, M(6, 1, 2) = $\{(\mu_2, \mu_4), (\mu_3, \mu_4), (\mu_3, \mu_5)\}$. Let A = $(\mu_{V_1}, \mu_{V_2}, \ldots, \mu_{V_{n-i-j-1}})$ denote a typical element of M(n, i, j). In essence, if we are given i infectives, the subscripts of the components of A represent a particular path followed to reach the state corresponding to n infectives. Since the end points, i and n, are always present, these subscripts are suppressed. For example, Figure 1 indicates the possible paths from i = 1 to n = 8 whenever j = 3 jumps of size 2 occur.

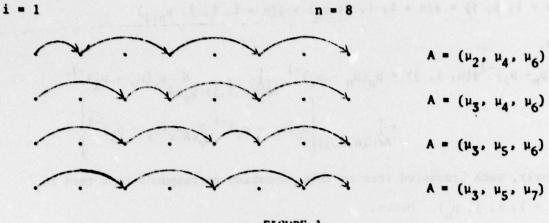


FIGURE 1

Paths for M(8, 1, 3)

Note that, in general, $j=0,1,\ldots, \lceil (n-i)/2 \rceil$ where $\lfloor x \rceil$ is the greatest integer less than or equal to x. Let us further define $M(n,i,j;\mu_{n-1})$ to be those elements A of M(n,i,j) such that $\mu_{n-1} \in A$, and let $M(n,i,j;\mu_{n-2})$ be similarly defined. Thus, in our example, $M(8,1,3;\mu_7)$ equals $\{(\mu_3,\mu_5,\mu_7)\}$ since only one path of M(8,1,3) contains μ_7 . Let

$$\phi(n, i, j) = \sum_{A \in M(n, i, j)} \prod_{\nu_{V} \in A} \mu_{\nu} / (\mu_{\nu} - \mu_{i})$$
 (3)

Finally, let $\phi(n, i, j; \mu_{n-1})$ be the sum of those terms of $\phi(n, i, j)$ that have μ_{n-1} as the factor of maximal subscript, with $\phi(n, i, j; \mu_{n-2})$ similarly defined.

Lemma 1

For distinct positive real numbers $\boldsymbol{\mu}_1,\;\dots,\;\boldsymbol{\mu}_n,$

$$\phi(n+1, i, j) = \mu_n (\mu_n - \mu_i)^{-1} \phi(n, i, j) + \mu_{n-1} (\mu_n - \mu_i)^{-1} \phi(n-1, i, j-1)$$
 (4) where $\phi(n, i, j)$ is defined as in (3).

Proof.

Since by definition the sets A of M(n + 1, i, j) cannot have both μ_n and μ_{n-1} deleted, it follows that

$$\phi(n+1, i, j) = \phi(n+1, i, j; \mu_n) + \phi(n+1, i, j; \mu_{n-1})$$
 (5)

Now .

$$\begin{split} \mu_{n}(\mu_{n}-\mu_{\underline{i}})^{-1}\phi(n,\,\underline{i},\,\underline{j}) &= \mu_{n}(\mu_{n}-\mu_{\underline{i}})^{-1} \sum_{\substack{A \in N(n,\underline{i},\underline{j}) \\ A \in N(n,\underline{i},\underline{j})}} \prod_{\substack{\mu_{V} \in A}} \mu_{V}(\mu_{V}-\mu_{\underline{i}})^{-1} \\ &= \sum_{\substack{A \in M(n,\underline{i},\underline{j})}} \left\{ \mu_{n}(\mu_{n}-\mu_{\underline{i}})^{-1} \prod_{\substack{\mu_{V} \in A}} \mu_{V}(\mu_{V}-\mu_{\underline{i}})^{-1} \right\}. \end{split}$$

Clearly, each bracketed term in this summation corresponds to a term in $\phi(n+1,i,j;\mu_n)$. Hence,

$$\mu_n(\mu_n - \mu_i)^{-1}\phi(n, i, j) = \phi(n + 1, i, j; \mu_n)$$
 (6)

Similarly, we can show

$$\mu_{n-1}(\mu_{n-1} - \mu_i)^{-1}\phi(n-1, i, j-1) = \phi(n+1, i, j; \mu_{n-1})$$

Thus, the result follows readily.

3. A SIMPLE BATCH EPIDEMIC

Let us now present the probability distribution of X(t) the number of infectives. Theorem 1

Consider a simple batch epidemic in a closed population of size N with transition probabilities as given in (1). Assume the parameters μ_i , $i=1,\ldots,N$ are distinct and that X(0)=1. Then, the probability distribution of the number of infectives present at time t is

$$p_n(t) = \sum_{i=1}^{n} d_{n,i} e^{-\mu_i t}, n = 1, ..., N$$
, (7)

whore

$$d_{1,1} = 1,$$

$$d_{n,i} = \frac{\mu_{i}d_{ii}}{\mu_{n} - \mu_{i}} \sum_{j=0}^{\lfloor (n-i)/2 \rfloor} (1 - \alpha)^{j}\alpha^{n-i-2j}\phi(n, i, j), \quad i = 2, ..., n - 1,$$

$$d_{n,n} = -\sum_{i=1}^{n-1} d_{n,i}, \quad n = 2, ..., N,$$
(8)

and where the $\phi(n, i, j)$ are defined in (3), and where $d_{n,m} \equiv 0$ whenever m > n.

Proof.

The result for n = 1 is clearly true.

We prove the result for n = 2, ..., N by induction. We first take n = 2. Substituting n = 2 into equation (2), we obtain

$$p_2(t) = [\alpha \mu_1/(\mu_2 - \mu_1)]e^{-\mu_1 t} - [\alpha \mu_1/(\mu_2 - \mu_1)]e^{-\mu_2 t}$$

Equation (8) implies the result is true for n = 2.

Now assume the result is true for $n=3,\ldots,n-1$. We wish to check the case n=n. Solving (2) for n=n, by using the integrating factor $\exp(\mu_n t)$, and (7) for n-1, n-2 we obtain

$$p_{n}(t) = \sum_{i=1}^{n-1} \left[\alpha \mu_{n-1} d_{n-1,i} + (1-\alpha) \mu_{n-2} d_{n-2,i}\right] / (\mu_{n} - \mu_{i}) e^{-\mu_{i}t}$$

$$+ \left\{ \sum_{i=1}^{n-1} \left[\alpha \mu_{n-1} d_{n-1,i} + (1-\alpha) \mu_{n-2} d_{n-2,i}\right] / (\mu_{n} - \mu_{i}) \right\} e^{-\mu_{n}t}$$
(9)

Thus, to prove the result, we need only show that the coefficient of $\exp(-\mu_i t)$ in (9) is indeed $d_{n,i}$. To do this we substitute for $d_{n-1,i}$ and $d_{n-2,i}$ using (8) which were assumed to be true. Let us assume n-i=2m+1 is odd. (The proof is analogous for n-i even). Thus, on a proper rearrangement of the terms, the coefficient of $\exp(-\mu_i t)$ becomes

$$\frac{\mu_{\mathbf{i}}^{\mathbf{d}}_{\mathbf{i}\mathbf{i}}}{\mu_{n} - \mu_{\mathbf{i}}} \left[\alpha^{n-\mathbf{i}} \frac{\mu_{n-1}}{\mu_{n-1} - \mu_{\mathbf{i}}} \phi(n-1, \mathbf{i}, \mathbf{o}) + \sum_{j=1}^{\lfloor (n-\mathbf{i})/2 \rfloor} (1-\alpha)^{j} \alpha^{n-\mathbf{i}-2j} \left\{ \frac{\mu_{n-1}}{\mu_{n-1} - \mu_{\mathbf{i}}} \phi(n-1, \mathbf{i}, \mathbf{j}) + \frac{\mu_{n-2}}{\mu_{n-2} - \mu_{\mathbf{i}}} \phi(n-2, \mathbf{i}, \mathbf{j}-1) \right\}$$

But, from (6) and (3), we have

$$\mu_{n-1}/(\mu_{n-1} - \mu_i)\phi(n-1, i, o) = \phi(n, i, o, \mu_n)$$

$$= \phi(n, i, o).$$
(10)

Substituting (10) and using Lemma 1, yields the result for n = n, and the theorem is proved.

Note that the coefficients $d_{n,i}$ satisfy the following recursive relationship $d_{n,i} = [\alpha \mu_{n-1} d_{n-1,i} + (1-\alpha) \mu_{n-2} d_{n-2,i}]/(\mu_n - \mu_i)$, i = 1, ..., N

with dn,m = o whenever m > n. This follows immediately from (9).

With the expressions for the probability distribution, we may now derive other quantities of interest, such as the mean number of infectives, duration time of the epidemic, the size of the epidemic, etc.

REFERENCES.

Billard, L., Lacayo, H. and Langberg, N. A. (1979). A new look at the simple epidemic process. J. Appl. Prob. 16, to appear.

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